

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 11:03:24 ; Search time 134 Seconds
(without alignments)
373.800 Million cell

updates/sec

Title: US-10-621-741A-1
Perfect score: 638
Sequence: 1 KPKEDREWEKFKTKHITSQS.....FICITCRDNYPVHFVKTGKC
114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

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OM protein - protein search, using sw model

Run on: January 26, 2006, 11:11:15 ; Search time 39 Seconds
(without alignments)
281.249 Million cell

updates/sec

Title: US-10-621-741A-1
Perfect score: 638

Sequence: 1 KPKEGREWEKFKTKHITSQS.....FICITCRDNYPVHFKTGKC
114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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OM protein - protein search, using sw model

Run on: January 26, 2006, 11:10:20 ; Search time 160 Seconds
(without alignments)
502.689 Million cell

updates/sec

Title: US-10-621-741A-1
Perfect score: 638
Sequence: 1 KPKEGREWEKFKTKHITSQS.....FICITCRDNYPVHFKTGKC
114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

AAB07489

XX

XX

XX

XX

XX

XX

FT Modified-site

FT Modified-site

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 100.0%; Score 638; DB 3; Length 114;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 KPKEGREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGOCKPINTFIHSTTGVPVEICR 60

Db 61 RATGRVNKSSTQOFTLTCKNPIRCKYSQSNTTNFICITCRDNYPVHFVKTGKC 114

ADW24080

XX

AC ADW24080;

XX
PD 20-JAN-2005.
XX
PF 17-JUL-2003; 2003US-00621741.
XX
PR 17-JUL-2003; 2003US-00621741.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Saxena SK;
XX
DR WPI; 2005-080949/09.
XX
PT New recombinantly produced ribonuclease, useful for treating tumors or
PT active against human carcinoma cells.
XX
PS Claim 8; SEQ ID NO 59; 32pp; English.
XX
CC The present invention relates to a method for recombinantly producing new
CC ribonuclease (RNases) protein. The invention is useful for treating
CC tumors and active against human carcinoma cells. The invention is also
CC useful in gene therapy. The present sequence is a Rana pipiens 2325p4
CC protein.
XX
SQ Sequence 115 AA;

Query Match 100.0%; Score 638; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKEGREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGPVKEICR 60
Db 2 KPKEGREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGPVKEICR 61
QY 61 RATGRVNKSSTQQFTLTTCNPIRCKYSQSNTTNFICITCRDNPVHFVKTGKC 114
Db 62 RATGRVNKSSTQQFTLTTCNPIRCKYSQSNTTNFICITCRDNPVHFVKTGKC 115

RESULT 4
ADW24141
ID ADW24141 standard; protein; 116 AA.
XX
AC ADW24141;
XX
DT 07-APR-2005 (first entry)
XX
DE Rana pipiens 2325p4 protein, seqid:63.
XX
KW Genetic engineering; ribonuclease; pharmaceutical; recombinant protein;
KW tumor; cytostatic; gene therapy; signal peptide.
XX
OS Rana pipiens.
XX
PN US2005014161-A1.
XX
PD 20-JAN-2005.
XX
PF 17-JUL-2003; 2003US-00621741.
XX
PR 17-JUL-2003; 2003US-00621741.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Saxena SK;
XX
DR WPI; 2005-080949/09.

XX ,
PT New recombinantly produced ribonuclease, useful for treating tumors or
PT active against human carcinoma cells.
XX
PS Claim 28; SEQ ID NO 63; 32pp; English.
XX
CC The present invention relates to a method for recombinantly producing new
CC ribonuclease (RNases) protein. The invention is useful for treating
CC tumors and active against human carcinoma cells. The invention is also
CC useful in gene therapy. The present sequence is a Rana pipiens 2325p4
CC protein.
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 638; DB 9; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 5

ADW24143

ID ADW24143 standard; protein; 121 AA.

XX

AC ADW24143;

XX

DT 07-APR-2005 (first entry)

XX

DE Rana pipiens 2325p4 protein, seqid:65.

XX

KW Genetic engineering; ribonuclease; pharmaceutical; recombinant protein;
KW tumor; cytostatic; gene therapy; signal peptide.

XX

OS *Rana pipiens*.

XX

PN US2005014161-A1.

XX

PD 20-JAN-2005.

XX

PF 17-JUL-2003; 2003US-00621741.

XX

PR 17-JUL-2003; 2003US-00621741.

XX

PA (ALFA-) ALFACELL CORP.

XX

PI Saxena SK;

XX

DR WPI; 2005-080949/09.

XX

PT New recombinantly produced ribonuclease, useful for treating tumors or
PT active against human carcinoma cells.

XX

PS Claim 29; SEQ ID NO 65; 32pp; English.

XX

CC The present invention relates to a method for recombinantly producing new
CC ribonuclease (RNases) protein. The invention is useful for treating
CC tumors and active against human carcinoma cells. The invention is also
CC useful in gene therapy. The present sequence is a Rana pipiens 2325p4
CC protein.

XX

SQ Sequence 121 AA;

Query Match 100.0%; Score 638; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.7e-63;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPKEDREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGPVKEICR 60
 |||
 Db 8 KPKEDREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGPVKEICR 67

Qy 61 RATGRVNKSSTQQFTLTTCNPIRCKYSQSNTTNFICITCRDNYPVHVKTGKC 114
 |||
 Db 68 RATGRVNKSSTQQFTLTTCNPIRCKYSQSNTTNFICITCRDNYPVHVKTGKC 121

RESULT 6
ADW24145

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ID      ADW24145 standard; protein; 136 AA.
XX
AC      ADW24145;
XX
DT      07-APR-2005    (first entry)
XX
DE      Rana pipiens 2325p4 protein, seqid:67.
XX
KW      Genetic engineering; ribonuclease; pharmaceutical; recombinant protein;
KW      tumor; cytostatic; gene therapy; signal peptide.
XX
OS      Rana pipiens.
XX
PN      US2005014161-A1.
XX
PD      20-JAN-2005.
XX
PF      17-JUL-2003; 2003US-00621741.
XX
PR      17-JUL-2003; 2003US-00621741.
XX
PA      (ALFA-) ALFACELL CORP.
XX
PI      Saxena SK;
XX
DR      WPI; 2005-080949/09.
XX
PT      New recombinantly produced ribonuclease, useful for treating tumors or
PT      active against human carcinoma cells.
XX
PS      Claim 30; SEQ ID NO 67; 32pp; English.
XX
CC      The present invention relates to a method for recombinantly producing new
CC      ribonuclease (RNases) protein. The invention is useful for treating
CC      tumors and active against human carcinoma cells. The invention is also
CC      useful in gene therapy. The present sequence is a Rana pipiens 2325p4
CC      protein.
XX
SQ      Sequence 136 AA;

```

Query Match 100.0%; Score 638; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 3.1e-63;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  KPKEGREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGPVKEICR  60
      |||
Db      23  KPKEGREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGPVKEICR  82
      |||
Qy      61  RATGRVNSSTQQFTLTTCNKPIRCKYSQSNTTNFICITCRDNYPVHVKTKGC  114
      |||

```

RESULT 1

US-09-223-118-1

; Sequence 1, Application US/09223118
 ; Patent No. 6239257
 ; GENERAL INFORMATION:
 ; APPLICANT: Ardelt Ph.D., Wojciech
 ; TITLE OF INVENTION: FAMILY OF PHARMACEUTICALS AND METHOD FOR MAKING IT
 ; FILE REFERENCE: 5010
 ; CURRENT APPLICATION NUMBER: US/09/223,118
 ; CURRENT FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 4.
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 114
 ; TYPE: PRT
 ; ORGANISM: Rana pipiens

US-09-223-118-1

Query Match 100.0%; Score 638; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 2.6e-65;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KPKEDREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGVPVKEICR	60
Db	1	KPKEDREWEKFKTKHITSQSVADFNCNRTMNDPAYTPDGQCKPINTFIHSTTGVPVKEICR	60
Qy	61	RATGRVNKSSTQQFTLTTCCKNPIRCKYSQSNTTNFICITCRDNYPVHFVKTGKC	114
Db	61	RATGRVNKSSTQQFTLTTCCKNPIRCKYSQSNTTNFICITCRDNYPVHFVKTGKC	114